

Application No.: 10/723,947 4
Response to OA of 10/3/2006; RCE; Extension of Time

Docket No.: 514112000320

REMARKS

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I. Status of Claims

Claim 1 has been amended and claims 38 and 39 have been added. Claims 24-37 have been canceled without prejudice. Applicants reserve the right to prosecute the canceled claims in a divisional application. Entry of this amendment is respectfully requested. After entry of this amendment, claims 1-23 and 38-39 will be pending.

The Amendment

In order to expedite prosecution of the application and advance the case toward allowance, the claims have been amended.

Claim 1 has been amended to specify an isolated nucleic acid that comprises a sequence having at least 95% identity to SEQ ID NO: 75. Claim 38 is directed to SEQ ID 75. Claim 39 is directed to SEQ ID 79. Support for this amendment can be found throughout the specification, in particular, at page 4 of the application as filed.

II. Withdrawal of Claims Directed to Nonelected Invention.

The Office Action indicates that the subject matter of claims 36 and 37 are withdrawn from consideration as being directed to a non-elected invention. Specifically, the Office Action alleges that claim 36 (drawn to SEQ ID NO: 79, 82, and 85) and claim 37 (drawn to SEQ ID NO: 82 and 85) are directed to inventions that are independent or distinct from the invention originally claimed. The Examiner reminds Applicants that nucleotide sequences encoding proteins are normally deemed to constitute independent and distinct inventions absent evidence to the contrary.

To the extent the rejection applies to the amended claim set, Applicants respectfully traverse. A restriction requirement is only proper if there would be a serious burden on the Examiner if restriction were not required. MPEP §803(I).

Applicants respectfully submit that no undue burden would be imposed by a search for claims directed to sequences. Claim 1 has been amended to specify an isolated nucleic acid that comprises a sequence having at least 95% identity to SEQ ID NO: 75. Claim 38 is directed to SEQ

sf-2261333 v3

Application No.: 10/723,947

5

Docket No.: 514112000320

Response to OA of 10/3/2006; RCE; Extension of Time

NO: ID 75. Claim 39 is directed to SEQ ID NO: 79. SEQ ID NO: 75 and SEQ ID NO: 79 have a 95.6% identity according to Needle, a global alignment program (see attached **EXHIBIT 1**). As such, since these two sequences have a demonstrated high degree of sequence identity, there is no additional burden on the Examiner in examining claims directed to both sequences, as a thorough search of art related to either sequence will necessarily turn up art related to the other sequence.

Furthermore, MPEP § 803.04 states, "It has been determined that normally ten sequences constitute a reasonable number for examination purposes. Accordingly, in most cases, up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction." Thus, the USPTO has determined that ten independent and distinct nucleotide sequences may be examined together, which could include sequences with extremely low levels of identity. In this case, the nucleic acid sequences have significant identity. Thus, under this special standard set forth in the MPEP for examination of nucleotide sequences, claims directed to all four sequences should be examined together.

Finally, the Examiner has already searched SEQ ID NO: 75. With this request for Continued Examination, applicant is entitled to a new search directed at SEQ ID NO: 79. Thus, as examination of claims directed to both sequences would not impose an undue burden on the Examiner and the two sequences meet the standard set forth in MPEP §803.04, Applicants request that the Examiner reconsider the request to withdraw claims drawn to sequences other than SEQ ID NO: 75 and examine claims directed to SEQ ID NO: 75 and 79 all together in this application.

III. Rejection Under 35 U.S.C. §112, second paragraph

Claims 1-27 are rejected under 35 U.S.C. §112, first paragraph, as allegedly being indefinite. The Examiner indicates that the sole designation of an amino acid sequence as "ZCCT1" is allegedly arbitrary and creates ambiguity and that an amendment of the claim to a specific SEQ ID NO would obviate this rejection.

As suggested by the Examiner, claim 1 has been amended to refer to specific sequence identifiers. Thus, the rejection should be moot and it is respectfully requested that the rejection be withdrawn.

sf-2261333 v3

Application No.: 10/723,947

6

Docket No.: 514112000320

Response to OA of 10/3/2006; RCE; Extension of Time

IV. Rejection Under 35 U.S.C. §112, first paragraph, written description

Claims 1-27 remain rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking written description. Specifically, the Office Action asserts that Applicants have allegedly not disclosed a structure/function relationship that demonstrates they are in full possession of the broadly claimed genus based on the definition of ZCCT1 protein, *i.e.*, ZCCT1 activity depends upon the intended use of the ZCCT1 protein.

To the extent the rejection applies to the amended claim set, Applicants respectfully traverse the rejection and its supporting remarks. According to *Eli Lilly*, the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by disclosure of relevant, identifying characteristics, *i.e.*, structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus. *See* 119 F.3d at 1568, 43 USPQ2d at 1406. In the present application, claim 1 has been amended to refer to sequences with 95% percent identity to SEQ ID NO: 75 and new claims 38 and 39 also recite SEQ ID NO:s 75 and 79, respectively. Therefore the claimed chemical genus is defined by structure. Furthermore, the specification discloses multiple representative species of the claimed genus of nucleic acids comprising nucleotide sequences with 95% identity to SEQ ID NO: 75. Paragraph 120 of the specification provides SEQ ID NO: 75 and paragraph 124 of the specification provides SEQ ID NO: 79, a sequence which is 95.6% identical to SEQ ID NO: 75 according to the Needle alignment program and cloned. See the attached alignment (EXHIBIT 1).

In view of the representative species disclosed in the specification, Applicants thus respectfully assert that a person of ordinary skill would recognize that Applicants had possession of the invention. Withdrawal of the rejection is respectfully requested.

sf-2261333 v3

Application No.: 10/723,947

7

Docket No.: 514112000320

Response to OA of 10/3/2006; RCE; Extension of Time

V. Rejection Under 35 U.S.C. §112, first paragraph, enablement

Claims 1-27 and 36 remain rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking enablement. The Examiner contends that Applicants' teaching on pages 81-83 of the specification disclosing methods for inhibiting expression of ZCCT1 in a wheat plant only provide enablement for the invention of Group II (drawn to plants containing constructs that inhibit expression of the ZCCT1), not for the invention of Group I (drawn to ZCCT1 sequences and methods comprising the ZCCT1 sequence). Furthermore, the Office Action asserts that the allegedly broad definition of ZCCT1 as any polypeptide that is able to interfere with the endogenous ZCCT1 activity and Applicants' disclosure of only full length sequences of SEQ ID NOS; 75 and 79, would allegedly not apprise one of skill of polypeptides that inhibit ZCCT1 activity that can be used in the elected invention. The Examiner concludes that undue trial and error would be required to make and or use the claimed invention.

To the extent the rejection applies to the amended claim set, Applicants respectfully traverse the rejection and its supporting remarks. Satisfaction of the enablement requires only that the specification teach a person of ordinary skill in the art how to make and use the invention. Working examples are not required. As indicated above, the amended and new claims refer to nucleic acids with 95 percent identity to SEQ ID NO: 75 (claims 1-5, 38-39); vectors, cells, transgenic plants, and transgenic seeds comprising these nucleic acids (claims 6-23). Two representative nucleic acids of this invention are explicitly taught in paragraphs 120 and 124 of the application. Methods for determining the nucleic acid sequence of other sequences with at least 95% identity to SEQ ID NO: 75 are taught in paragraphs 90 to 96. Finally, methods for making vectors, cells, transgenic plants, and transgenic seeds are both well known to those of skill in the art and also taught in the specification in the sections entitled "Vectors" (starting at para. 148) and "Transgenic Plants" (para. 156).

Claims to methods for altering the vernalization phenotype by transforming a plant with a genetic construct comprising the isolated nucleic acids of the invention have been canceled.

sf-2261333 v3

MAR 26 2007

Application No.: 10/723,947

8

Docket No.: 514112000320

Response to OA of 10/3/2006; RCE; Extension of Time

As such, undue experimentation is not required for one of skill in the art to make and use the invention. Applicants thus respectfully assert that the claimed invention is fully enabled and request withdrawal of the rejection.

CONCLUSION

In view of the above, each of the presently pending claims in this application is believed to be in immediate condition for allowance. Accordingly, the Examiner is respectfully requested to withdraw the outstanding rejection of the claims and to pass this application to issue. If it is determined that a telephone conference would expedite the prosecution of this application, the Examiner is invited to telephone the undersigned at the number given below.

In the event the U.S. Patent and Trademark office determines that an extension and/or other relief is required, applicant petitions for any required relief including extensions of time and authorizes the Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to Deposit Account No. 03-1952 referencing docket no. 514112000320. However, the Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: March 26, 2007

By


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Registration No.: 38,651

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sf-2261333 v3

EXHIBIT 1

4homology

EMBOSS Align Results

Needle Results

Matrix DNafull

Open gap penalty 10.0

Gap extension penalty 0.5

Needle output needle-20070207-05223824974575.output

#####

Program: needle

Rndate: Wed Feb 07 05:22:38 2007

Align_format: srspair

Report_file: /ebi/extserv/old-work/needle-20070207-05223824974575.output

#####

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#

Aligned_sequences: 2

1: EMBOSS_001

2: EMBOSS_001

Matrix: EDNAFULL

Gap_penalty: 10.0

Extend_penalty: 0.5

#

Length: 996

Identity: 952/996 (95.6%)

Similarity: 952/996 (95.6%)

Gaps: 21/996 (2.1%)

Score: 4648.0

#

#

#

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EMBOSS_001      1 taactgcctcttcttcttctcctcgacgtctctcctcctcggtcctccacg      50
EMBOSS_001      1 taactgcctcttcttcttctcctcgacatctctcctcctcggtcttctccacg      50
EMBOSS_001     51 caccagaccacaccagaaaaaacaagaagcaaaccttgagctag      100
EMBOSS_001     51 caccagaccacagcagaaaaaacaagaagcaaaccttgagctag      100
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EMBOSS_001    280 gaccatagcagaacatggaccacaccatttcatgaaacagcagctgcagg      329
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4homology

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EMBOSS_001	401	ctcacctagtgcagccaccggcaagagcccaacatcgtgccattttcacgga	450
EMBOSS_001	380	ctcacctagtgcagccaccggcaagagcccaacatcgtgccattttacgga	429
EMBOSS_001	451	ggtgcattcaccaacactattagcaatgaagcaatcatgactattgacac	500
EMBOSS_001	430	ggtgcattcaccaacactattagcaatgaagcaatcatgactattgacac	479
EMBOSS_001	501	agagatgatgggtggggcctgcccattatcccacaatgcaggagagagcag	550
EMBOSS_001	480	agagatgatgggtggggcctgcccattatcccacaatgcaggagagagcag	529
EMBOSS_001	551	cgaaggatgatgagggtatagggagaagaggaagaggcggtatgacaag	600
EMBOSS_001	530	cgaaggatgatgagggtatagggagaagaggaagaggcggtatgacaag	579
EMBOSS_001	601	caaaccgatacagagtcagaaaagcttacgctgagcttcggccatgggt	650
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EMBOSS_001	701	cagcttcgcccctatgatcctagtaaacttcacctcggatggttccggtaa	750
EMBOSS_001	680	cagcttcgcccctatgatcctagtaaacttcacctcggatggttccggtaa	729
EMBOSS_001	751	tttatagcacaagccagataaaatgataacatatttccttctgattgac	800
EMBOSS_001	730	tttatagcacaagccagataaaatgataacatatttccttctgattgac	779
EMBOSS_001	801	caccggtgaagcagttgttcctcaagtaaaataagtcggttagtgattg	850
EMBOSS_001	780	caccggtgaagcagttgttcctcaagtaaaataagtcggttagtgattg	829
EMBOSS_001	851	atcgattggagccattatgttgacttgactattttaaataaggtcagcagat	900
EMBOSS_001	830	atcgattggagccattatgttgacttgactattttaaataaggtcagcagat	879
EMBOSS_001	901	caatcaaaacaaaatgtattttattgaaacaagtcttgttatactacgtgtt	950
EMBOSS_001	880	caatcaaaacaaaatgtattttattgaaacaagtcttgttatactacgtgtt	929
EMBOSS_001	951	gattttaaacaatgtaattttcaagaggatagctactttgatgtgtaat	996
EMBOSS_001	930	gattttaaacaatgtaattttcaagaggatagctactttgatgtgtaat	975

EMBOSS Align Results

Needle Results

Matrix DNAsfull

Open gap penalty 10.0

Gap extension penalty 0.5

Needle output needle-20070207-05300387024182.output